

Nowadays, **Macromolecular crystallography (MX)** is one of the most important research areas providing essential information to the rationalization of cellular molecular mechanisms and with practical application in other research fields, such as rational drug design, bio- and nanotechnological areas. As an example, while studying a protein target known to be essential in the development of a particular disease, the extensive analysis of the protein crystal structure will provide molecular clues for the development of a specific drug therefore defining novel therapeutic strategies. MX can also be important in protein design, where starting from a known protein structure, a modified version is obtained by making calculated structural variations aiming the enhancement of a specific function. The Macromolecular Crystallography Unit at ITQB is organized into four different Laboratories: Structural Genomics, Structural Biology, Industry and Medicine Applied Crystallography and Membrane Protein Crystallography. Different projects are currently underway in our Unit (<http://xtal.itqb.unl.pt>) and the methodologies used can be summarized into five stages: gene cloning, protein expression, purification and crystallization, structure determination, refinement and analysis. For some projects, the target proteins are cloned, expressed and purified within the Unit, whereas for others the purified protein is supplied by other research Laboratories, either from ITQB or outside, within the framework of collaboration projects. Our main goal is to determine the crystal structures of the protein targets under study, in order to understand the molecular processes in which those proteins are key players.